

## SEQUENCE LISTING

<110> WU, TZZY-CHOOU  
HUNG, CHIEN, FU

<120> ANTI-CANCER DNA VACCINE EMPLOYING PLASMIDS ENCODING SIGNAL SEQUENCE, MUTANT ONCOPROTEIN ANTIGEN, AND HEAT SHOCK PROTEIN

<130> JHV-050.01 (19546-5001)

<140> 10/555,669  
<141> 2004-05-05

<150> PCT/US04/013756  
<151> 2004-05-05

<150> 60/467,602  
<151> 2003-05-05

<160> 20

<170> PatentIn Ver. 3.3

<210> 1  
<211> 297  
<212> DNA  
<213> Human papillomavirus

<220>  
<221> CDS  
<222> (1)..(297)

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atg cat gga gat aca cct aca ttg cat gaa tat atg tta gat ttg caa 48  
Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln  
1 5 10 15

cca gag aca act gat ctc tac tgt tat gag caa tta aat gac agc tca 96  
Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser  
20 25 30

gag gag gag gat gaa ata gat ggt cca gct gga caa gca gaa ccg gac 144  
Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp  
35 40 45

aga gcc cat tac aat att gta acc ttt tgt tgc aag tgt gac tct acg 192  
Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr  
50 55 60

ctt cgg ttg tgc gta caa agc aca cac gta gac att cgt act ttg gaa 240  
Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu  
65 70 75 80

gac ctg tta atg ggc aca cta gga att gtg tgc ccc atc tgt tct cag 288  
Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln  
85 90 95

gat aag ctt  
Asp Lys Leu

297

<210> 2  
<211> 99  
<212> PRT  
<213> Human papillomavirus

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Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln  
1 5 10 15  
Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser  
20 25 30  
Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp  
35 40 45  
Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr  
50 55 60  
Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu  
65 70 75 80  
Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln  
85 90 95  
Asp Lys Leu

<210> 3  
<211> 98  
<212> PRT  
<213> Human papillomavirus

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Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln  
1 5 10 15  
Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser  
20 25 30  
Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp  
35 40 45  
Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr  
50 55 60  
Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu  
65 70 75 80  
Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln  
85 90 95  
Lys Pro

<210> 4  
 <211> 158  
 <212> PRT  
 <213> Human papillomavirus

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 Arg Lys Leu Pro Gln Leu Cys Thr Glu Leu Gln Thr Thr Ile His Asp  
     20                 25                 30  
 Ile Ile Leu Glu Cys Val Tyr Cys Lys Gln Gln Leu Leu Arg Arg Glu  
     35                 40                 45  
 Val Tyr Asp Phe Ala Phe Arg Asp Leu Cys Ile Val Tyr Arg Asp Gly  
     50                 55                 60  
 Asn Pro Tyr Ala Val Cys Asp Lys Cys Leu Lys Phe Tyr Ser Lys Ile  
     65                 70                 75                 80  
 Ser Glu Tyr Arg His Tyr Cys Tyr Ser Leu Tyr Gly Thr Thr Leu Glu  
     85                 90                 95  
 Gln Gln Tyr Asn Lys Pro Leu Cys Asp Leu Leu Ile Arg Cys Ile Asn  
     100                 105                 110  
 Cys Gln Lys Pro Leu Cys Pro Glu Glu Lys Gln Arg His Leu Asp Lys  
     115                 120                 125  
 Lys Gln Arg Phe His Asn Ile Arg Gly Arg Trp Thr Gly Arg Cys Met  
     130                 135                 140  
 Ser Cys Cys Arg Ser Ser Arg Thr Arg Arg Glu Thr Gln Leu  
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<210> 5  
 <211> 151  
 <212> PRT  
 <213> Human papillomavirus

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 Thr Glu Leu Gln Thr Thr Ile His Asp Ile Ile Leu Glu Cys Val Tyr  
     20                 25                 30  
 Cys Lys Gln Gln Leu Leu Arg Arg Glu Val Tyr Asp Phe Ala Phe Arg  
     35                 40                 45  
 Asp Leu Cys Ile Val Tyr Arg Asp Gly Asn Pro Tyr Ala Val Cys Asp  
     50                 55                 60

Lys Cys Leu Lys Phe Tyr Ser Lys Ile Ser Glu Tyr Arg His Tyr Cys  
 65 70 75 80

Tyr Ser Leu Tyr Gly Thr Thr Leu Glu Gln Gln Tyr Asn Lys Pro Leu  
 85 90 95

Cys Asp Leu Leu Ile Arg Cys Ile Asn Cys Gln Lys Pro Leu Cys Pro  
 100 105 110

Glu Glu Lys Gln Arg His Leu Asp Lys Lys Gln Arg Phe His Asn Ile  
 115 120 125

Arg Gly Arg Trp Thr Gly Arg Cys Met Ser Cys Cys Arg Ser Ser Arg  
 130 135 140

Thr Arg Arg Glu Thr Gln Leu  
 145 150

&lt;210&gt; 6

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Human papillomavirus

&lt;400&gt; 6

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 tataatgttag atttgcacc agagacaact gatctctact gttatgagca attaaatgac 180  
 agctcagagg aggaggatga aatagatggt ccagctggac aagcagaacc ggacagagcc 240  
 cattacaata ttgtaacctt ttgttgcag tttgactcta cgcttcgggtt gtgcgtacaa 300  
 agcacacacg tagacattcg tactttggaa gacctgttaa tgggcacact aggaattgtg 360  
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&lt;210&gt; 7

&lt;211&gt; 127

&lt;212&gt; PRT

&lt;213&gt; Human papillomavirus

&lt;400&gt; 7

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Gly Leu Ala His Gly Ala Ser Ala Leu Phe Glu Asp Leu Ile Met His  
 20 25 30

Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln Pro Glu  
 35 40 45

Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser Glu Glu  
 50 55 60

Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp Arg Ala  
 65 70 75 80

His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr Leu Arg  
 85 90 95

Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu Asp Leu  
 100 105 110

Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln Pro  
 115 120 125

<210> 8  
 <211> 90  
 <212> DNA  
 <213> Human papillomavirus

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 ggcgcctcag cactcttga ggatctaattc 90

<210> 9  
 <211> 1878  
 <212> DNA  
 <213> Mycobacterium tuberculosis

<400> 9  
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 gcgttcgccc gcaacggatga ggtgctggtc ggcagcccg ccaagaacca ggcagtgacc 180  
 aacgtcgatc gcaccgtgcg ctggatcaag cgacacatgg gcagcgactg gtccatagag 240  
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 cgcgacgccc aggcttaccc cggtgaggac attaccgacg cggttatcac gacgcccccc 360  
 tacttcaatg acggcccgatc tcaggccacc aaggacgccc gccagatcgc cggcctcaac 420  
 gtgctcgatc tcgtcaacgc gccgaccgcg gccggcgctgg cctacggctc cgacaaggcc 480  
 gagaaggagc agcaaatctt ggtcttcgc ttgggtgtt gcacttgcg cgtttccctg 540  
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 atcactcagg acctgatcgatcc cccgactcgatcc aaggccgttcc agtcggatcgat cgctgacacc 900  
 ggcatttcgg tgcggatcgat cgatcacgtt gtgtcgatcgat gttggatcgac cccgatgccc 960  
 gcggtgaccgc atctggatcc ggaactcacc ggcggcaagg aacccaaacaa gggcgatcaac 1020  
 cccgatcgatcc ttgtcgatcgatcc gggagcccgat ctgcaggccg gcgtcctcaatc gggcgaggtg 1080  
 aaagacgttc tgctcgatcgat tggatcccg ctgaggatcgat gtttggatcgat ccacccgggg 1140  
 gtgatgatcgat ccgtcgatcgat ggcacacacc acgatcccgat ccaagcgatcgat ggagactttc 1200  
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 gagaaggatcgatcc tcaaaatcgatcc gctgtggatcgatcc gagggatcgatcc cgaaggatcgatcc tgaagacacccg 1620  
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 ccggccggatcgatcc cccaccccgat ccgttgcgtatcc gaggttggatcgatcc acgcccggatcgatcc ggtcgacccg 1860  
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 <211> 625  
 <212> PRT  
 <213> *Mycobacterium tuberculosis*

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       20                  25                  30

Ser Arg Thr Thr Pro Ser Ile Val Ala Phe Ala Arg Asn Gly Glu Val  
       35                  40                  45

Leu Val Gly Gln Pro Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg  
       50                  55                  60

Thr Val Arg Ser Val Lys Arg His Met Gly Ser Asp Trp Ser Ile Glu  
       65                  70                  75                  80

Ile Asp Gly Lys Lys Tyr Thr Ala Pro Glu Ile Ser Ala Arg Ile Leu  
       85                  90                  95

Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Ile Thr  
       100                  105                  110

Asp Ala Val Ile Thr Thr Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln  
       115                  120                  125

Ala Thr Lys Asp Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile  
       130                  135                  140

Val Asn Glu Pro Thr Ala Ala Leu Ala Tyr Gly Leu Asp Lys Gly  
       145                  150                  155                  160

Glu Lys Glu Gln Arg Ile Leu Val Phe Asp Leu Gly Gly Thr Phe  
       165                  170                  175

Asp Val Ser Leu Leu Glu Ile Gly Glu Gly Val Val Glu Val Arg Ala  
       180                  185                  190

Thr Ser Gly Asp Asn His Leu Gly Gly Asp Asp Trp Asp Gln Arg Val  
       195                  200                  205

Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Ile Asp Leu  
       210                  215                  220

Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys  
       225                  230                  235                  240

Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro  
       245                  250                  255

Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln  
       260                  265                  270

Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Asp Arg  
 275 280 285  
 Thr Arg Lys Pro Phe Gln Ser Val Ile Ala Asp Thr Gly Ile Ser Val  
 290 295 300  
 Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro  
 305 310 315 320  
 Ala Val Thr Asp Leu Val Lys Glu Leu Thr Gly Gly Lys Glu Pro Asn  
 325 330 335  
 Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln  
 340 345 350  
 Ala Gly Val Leu Lys Gly Glu Val Lys Asp Val Leu Leu Asp Val  
 355 360 365  
 Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Arg  
 370 375 380  
 Leu Ile Glu Arg Asn Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe  
 385 390 395 400  
 Thr Thr Ala Asp Asp Asn Gln Pro Ser Val Gln Ile Gln Val Tyr Gln  
 405 410 415  
 Gly Glu Arg Glu Ile Ala Ala His Asn Lys Leu Leu Gly Ser Phe Glu  
 420 425 430  
 Leu Thr Gly Ile Pro Pro Ala Pro Arg Gly Ile Pro Gln Ile Glu Val  
 435 440 445  
 Thr Phe Asp Ile Asp Ala Asn Gly Ile Val His Val Thr Ala Lys Asp  
 450 455 460  
 Lys Gly Thr Gly Lys Glu Asn Thr Ile Arg Ile Gln Glu Gly Ser Gly  
 465 470 475 480  
 Leu Ser Lys Glu Asp Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His  
 485 490 495  
 Ala Glu Glu Asp Arg Lys Arg Arg Glu Glu Ala Asp Val Arg Asn Gln  
 500 505 510  
 Ala Glu Thr Leu Val Tyr Gln Thr Glu Lys Phe Val Lys Glu Gln Arg  
 515 520 525  
 Glu Ala Glu Gly Gly Ser Lys Val Pro Glu Asp Thr Leu Asn Lys Val  
 530 535 540  
 Asp Ala Ala Val Ala Glu Ala Lys Ala Ala Leu Gly Gly Ser Asp Ile  
 545 550 555 560  
 Ser Ala Ile Lys Ser Ala Met Glu Lys Leu Gly Gln Glu Ser Gln Ala  
 565 570 575

Leu Gly Gln Ala Ile Tyr Glu Ala Ala Gln Ala Ala Ser Gln Ala Thr  
 580 585 590

Gly Ala Ala His Pro Gly Gly Glu Pro Gly Gly Ala His Pro Gly Ser  
 595 600 605

Ala Asp Asp Val Val Asp Ala Glu Val Val Asp Asp Gly Arg Glu Ala  
 610 615 620

Lys  
 625

<210> 11  
 <211> 2104  
 <212> DNA  
 <213> Artificial Sequence

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<221> CDS  
 <222> (1)..(2103)

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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cca gag aca act gat ctc tac tgt tat gag caa tta aat gac agc tca 96  
 Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser  
 20 25 30

gag gag gag gat gaa ata gat ggt cca gct gga caa gca gaa ccg gac 144  
 Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp  
 35 40 45

aga gcc cat tac aat att gta acc ttt tgt tgc aag tgt gac tct acg 192  
 Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr  
 50 55 60

ctt cgg ttg tgc gta caa agc aca cac gta gac att cgt act ttg gaa 240  
 Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu  
 65 70 75 80

gac ctg tta atg ggc aca cta gga att gtg tgc ccc atc tgt tct caa 288  
 Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln  
 85 90 95

gga tcc atg gct cgt gcg gtc ggg atc gac ctc ggg acc acc aac tcc 336  
 Gly Ser Met Ala Arg Ala Val Gly Ile Asp Leu Gly Thr Thr Asn Ser  
 100 105 110

gtc gtc tcg gtt ctg gaa ggt ggc gac ccg gtc gtc gtc gcc aac tcc 384  
 Val Val Ser Val Leu Glu Gly Gly Asp Pro Val Val Val Ala Asn Ser  
 115 120 125

gag ggc tcc agg acc acc ccg tca att gtc gcg ttc gcc cgc aac ggt	432		
Glu Gly Ser Arg Thr Thr Pro Ser Ile Val Ala Phe Ala Arg Asn Gly			
130	135	140	
gag gtg ctg gtc ggc cag ccc gcc aag aac cag gca gtg acc aac gtc	480		
Glu Val Leu Val Gly Gln Pro Ala Lys Asn Gln Ala Val Thr Asn Val			
145	150	155	160
gat cgc acc gtg cgc tcg gtc aag cga cac atg ggc agc gac tgg tcc	528		
Asp Arg Thr Val Arg Ser Val Lys Arg His Met Gly Ser Asp Trp Ser			
165	170	175	
ata gag att gac ggc aag aaa tac acc gcc ccg gag atc agc gcc cgc	576		
Ile Glu Ile Asp Gly Lys Lys Tyr Thr Ala Pro Glu Ile Ser Ala Arg			
180	185	190	
att ctg atg aag ctg aag cgc gac gcc gag gcc tac ctc ggt gag gac	624		
Ile Leu Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp			
195	200	205	
att acc gac gcg gtt atc acg acg ccc gcc tac ttc aat gac gcc cag	672		
Ile Thr Asp Ala Val Ile Thr Thr Pro Ala Tyr Phe Asn Asp Ala Gln			
210	215	220	
cgt cag gcc acc aag gac gcc ggc cag atc gcc ggc ctc aac gtc ctg	720		
Arg Gln Ala Thr Lys Asp Ala Gly Gln Ile Ala Gly Leu Asn Val Leu			
225	230	235	240
cgg atc gtc aac gag ccg acc gcg gcc ggc ctg gcc tac ggc ctc gac	768		
Arg Ile Val Asn Glu Pro Thr Ala Ala Leu Ala Tyr Gly Leu Asp			
245	250	255	
aag ggc gag aag gag cag cga atc ctg gtc ttc gac ttg ggt ggt ggc	816		
Lys Gly Glu Lys Glu Gln Arg Ile Leu Val Phe Asp Leu Gly Gly Gly			
260	265	270	
act ttc gac gtt tcc ctg ctg gag atc ggc gag ggt gtc gtt gag gtc	864		
Thr Phe Asp Val Ser Leu Leu Glu Ile Gly Glu Gly Val Val Glu Val			
275	280	285	
cgt gcc act tcg ggt gac aac cac ctc ggc ggc gac gac tgg gac cag	912		
Arg Ala Thr Ser Gly Asp Asn His Leu Gly Gly Asp Asp Trp Asp Gln			
290	295	300	
cggt gtc gtc gat tgg ctg gtc gac aag ttc aag ggc acc agc ggc atc	960		
Arg Val Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Ile			
305	310	315	320
gat ctg acc aag gac aag atg gcg atg cag cgg ctg cgg gaa gcc gcc	1008		
Asp Leu Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala			
325	330	335	
gag aag gca aag atc gag ctg agt tcg agt cag tcc acc tcg atc aac	1056		
Glu Lys Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn			
340	345	350	

ctg ccc tac atc acc gtc gac gcc gac aag aac ccg ttg ttc tta gac	1104
Leu Pro Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp	
355 360 365	
gag cag ctg acc cgc gcg gag ttc caa cggttccactcactcag gac ctg ctg	1152
Glu Gln Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu	
370 375 380	
gac cgc act cgc aag ccg ttc cag tcg gtg atc gct gac acc ggc att	1200
Asp Arg Thr Arg Lys Pro Phe Gln Ser Val Ile Ala Asp Thr Gly Ile	
385 390 395 400	
tcg gtg tcg gag atc gat cac gtt gtg ctc gtg ggt ggt tcg acc ccg	1248
Ser Val Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg	
405 410 415	
atg ccc gcg gtg acc gat ctg gtc aag gaa ctc acc ggc ggc aag gaa	1296
Met Pro Ala Val Thr Asp Leu Val Lys Glu Leu Thr Gly Gly Lys Glu	
420 425 430	
ccc aac aag ggc gtc aac ccc gat gag gtt gtc gcg gtg gga gcc gct	1344
Pro Asn Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala	
435 440 445	
ctg cag gcc ggc gtc ctc aag ggc gag gtg aaa gac gtt ctg ctg ctt	1392
Leu Gln Ala Gly Val Leu Lys Gly Glu Val Lys Asp Val Leu Leu Leu	
450 455 460	
gat gtt acc ccg ctg agc ctg ggt atc gag acc aag ggc ggg gtg atg	1440
Asp Val Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met	
465 470 475 480	
acc agg ctc atc gag cgc aac acc acg atc ccc acc aag ccg tcg gag	1488
Thr Arg Leu Ile Glu Arg Asn Thr Ile Pro Thr Lys Arg Ser Glu	
485 490 495	
act ttc acc acc gcc gac gac aac caa ccg tcg gtg cag atc cag gtc	1536
Thr Phe Thr Thr Ala Asp Asp Asn Gln Pro Ser Val Gln Ile Gln Val	
500 505 510	
tat cag ggg gag cgt gag atc gcc gcg cac aac aag ttg ctc ggg tcc	1584
Tyr Gln Gly Glu Arg Glu Ile Ala Ala His Asn Lys Leu Leu Gly Ser	
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ttc gag ctg acc ggc atc ccg ccg gcg ccg ccg ggg att ccg cag atc	1632
Phe Glu Leu Thr Gly Ile Pro Pro Ala Pro Arg Gly Ile Pro Gln Ile	
530 535 540	
gag gtc act ttc gac atc gac gcc aac ggc att gtg cac gtc acc gcc	1680
Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Val His Val Thr Ala	
545 550 555 560	
aag gac aag ggc acc ggc aag gag aac acg atc cga atc cag gaa ggc	1728
Lys Asp Lys Gly Thr Gly Lys Glu Asn Thr Ile Arg Ile Gln Glu Gly	
565 570 575	

tcg ggc ctg tcc aag gaa gac att gac cgc atg atc aag gac gcc gaa	1776
Ser Gly Leu Ser Lys Glu Asp Ile Asp Arg Met Ile Lys Asp Ala Glu	
580 585 590	
gcg cac gcc gag gag gat cgc aag cgt cgc gag gag gcc gat gtt cgt	1824
Ala His Ala Glu Glu Asp Arg Lys Arg Arg Glu Glu Ala Asp Val Arg	
595 600 605	
aat caa gcc gag aca ttg gtc tac cag acg gag aag ttc gtc aaa gaa	1872
Asn Gln Ala Glu Thr Leu Val Tyr Gln Thr Glu Lys Phe Val Lys Glu	
610 615 620	
cag cgt gag gcc gag ggt ggt tcg aag gta cct gaa gac acg ctg aac	1920
Gln Arg Glu Ala Glu Gly Ser Lys Val Pro Glu Asp Thr Leu Asn	
625 630 635 640	
aag gtt gat gcc gcg gtg gcg gaa gcg aag gcg gca ctt ggc gga tcg	1968
Lys Val Asp Ala Ala Val Ala Glu Ala Lys Ala Ala Leu Gly Gly Ser	
645 650 655	
gat att tcg gcc atc aag tcg gcg atg gag aag ctg ggc cag gag tcg	2016
Asp Ile Ser Ala Ile Lys Ser Ala Met Glu Lys Leu Gly Gln Glu Ser	
660 665 670	
cag gct ctg ggg caa gcg atc tac gaa gca gct cag gct gcg tca cag	2064
Gln Ala Leu Gly Gln Ala Ile Tyr Glu Ala Ala Gln Ala Ala Ser Gln	
675 680 685	
gcc act ggc gct gcc cac ccc ggc tcg gct gat gaa agc a	2104
Ala Thr Gly Ala Ala His Pro Gly Ser Ala Asp Glu Ser	
690 695 700	
<210> 12	
<211> 701	
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<400> 12	
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Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp	
35 40 45	
Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr	
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Pro Asn Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala  
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